

IN THE CLAIMS:

WHAT IS CLAIMED IS:

1. (Currently Amended) A method for identifying the presence of a bacterium in a sample comprising
 - a) testing said sample by Gram-staining and ~~determining the rod or coccus character of said bacterium and when said Gram-staining indicates the presence of a Gram-positive bacterium with a coccus character, further determining a chain-like or clump-like character of said bacterium,~~
 - b) testing said sample with a probe according to an *in situ* hybridisation protocol selected on the basis of ~~the outcome of said Gram-staining, said method further comprising~~
 - (i) ~~when said Gram-staining indicates the presence of a Gram-negative bacterium with a coccus character, subjecting said sample to a treatment with a lysis buffer comprising lysozyme, and~~
 - (ii) ~~when said Gram-staining indicates the presence of a Gram-positive bacterium with a rod character, subjecting said sample to a treatment with a lysis buffer comprising lysozyme and/or Proteinase K, and~~
 - (iii) ~~when said Gram-staining indicates the presence of a Gram-positive bacterium with a coccus and chain-like character subjecting said sample to a treatment with a lysis buffer comprising lysozyme and,~~
 - (iv) ~~when said Gram-staining indicates the presence of a Gram-positive bacterium with a coccus and clump-like character subjecting said sample to a treatment with a lysis buffer comprising lysostaphin and/or Proteinase K, whether the Gram staining indicates the presence of a Gram negative or Gram positive staining~~and identifying the presence of the bacterium in the sample.
2. (Previously Presented) A method according to claim 1 wherein said sample is a clinical sample.
3. (Currently Amended) A method according to claim 2 wherein said sample is mammalian blood.
4. (Canceled)
5. (Currently Amended) A method according to claim 1~~4~~ wherein said character is of the ~~Gram-negative~~ rod type, further comprising hybridising said sample with at least one probe

selected from a group of probes for detecting nucleic acid found in an organism selected from the a group consisting of *Escherichia coli*, *Klebsiella pneumoniae*, *Klebsiella oxytoca*, *Serratia marcescens*, *Enterobacter aerogenes*, *Enterobacter cloacae*, *Proteus vulgaris*, *Proteus mirabilis*, *Salmonella typhi*, and *Pseudomonas aeruginosa*.

6. (Previously Presented) A method according to claim 5 wherein said nucleic acid is ribosomal RNA.

7. (Currently Amended) A method according to claim 6 wherein said probe is ~~having no more than five, preferably no more than two mismatches with a probe~~ is selected ~~of from~~ a the group consisting of

GCCTGCCAGTTTCGAATG (SEQ ID NO:1) or

GTAGCCCTACTCGTAAGG (SEQ ID NO:2) or

GAGCAAAGGTATTAACCTTTACTCCC (SEQ ID NO:3) or

GTTAGCCGTCCCTTTCTGG (SEQ ID NO:4).

8-12 (Canceled)

13. (Currently Amended) A method according to claim ~~12~~1, wherein said character is of a Gram-positive chain-like coccus type further comprising hybridising said sample with at least one probe selected from a group consisting of probes for detecting nucleic acid found in an organism selected from the group consisting of *Enterococcus faecalis*, *Streptococcus pneumoniae*, *Streptococcus mitis*, *Streptococcus viridans*, *Streptococcus sanguis*, and *Enterococcus faecium*.

14. (Previously Presented) A method according to claim 13 wherein said nucleic acid is ribosomal RNA.

15. (Currently Amended) A method according to claim 14 wherein said probe is ~~having no more than five mismatches with a probe selected from the of a~~ group composed of probes ~~having a sequence consisting of~~ TTATCCCCCTCTGATGGG (SEQ ID NO:5) or AGAGAAGCAAGCTTCTCGTCCG (SEQ ID NO:6) or GCCACTCCTCTTTTCCGG (SEQ ID NO:7).

16. (Canceled)

17. (Currently Amended) A method according to claim ~~16~~1, wherein said character is of a Gram-positive clumb-like coccus type further comprising hybridising said sample with at least one probe selected from a group consisting of probes for detecting nucleic acid found in an

organism selected from the a group consisting of *Staphylococcus aureus*, *Staphylococcus haemolyticus*, and *Staphylococcus saprophyticus*.

18. (Previously Presented) A method according to claim 17 wherein said nucleic acid is ribosomal RNA.

19. (Currently Amended) A method according to claim 18 wherein said probe is ~~having no more than five mismatches with a probe selected offrom thea~~ group consisting of probes ~~having a sequence~~ GCTAATGCAGCGCGGATCC (SEQ ID NO:8) or CCGAAGGGGAAGGCTCTA (SEQ ID NO:9) or AGAGAAGCAAGCTTCTCGTCCGTT (SEQ ID NO:10).

20. (Previously Presented) A method according to claim 1 further comprising hybridising said sample with at least one positive control probe and/or with at least one negative control probe.

21. (Currently Amended) A method according to claim 20 wherein said positive control probe ~~comprises no more than five mismatches with a probe with the~~ consists of the sequence GCTGCCTCCCGTAGGAGT (SEQ ID NO:11) and/or wherein said negative control probe ~~comprises no more than five mismathces with a probe with the~~ consists of the sequence ACTCCTACGGGAGGCAGC (SEQ ID NO:12).

22. (Previously Presented) A method according to claim 1 further comprising a one-step procedure of binding bacteria present in said sample to a microscopic slide and simultaneously fixing intracellular structures.